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(54) Title: METHOD FOR AUTOMATED, LARGE-SCALE MEASUREMENT OF THE MOLECULAR FLUX RATES OF THE PROTEOME OR THE ORGANEOME USING MASS SPECTROMETRY

stable isotope Total Cellular Proteins administration (in vivo) **Enzymatic** hydrolysis Complex mixture of peptides (~5-25-mers) chromatography (stepped gradient) Partially resolved peptides MS (#1) mass analysis Ion fragments, sorted Argon; MS Secondary fragments L mass analysis Characteristic MW's and fingerprint of sequence Isotopomer Informatic analysis Biosynthetic and Total catabolic rates expressed Informatics proteome content Dynamic proteome Current (static) Dynamic **Proteomics Proteomics** 

(57) Abstracts Disclosed here is a method for measuring the kinetics (i.e., the molecular flux rates - synthesis and breakdown or removal rates) of a plurality of proteins or organic metabolites inn living systems. The methods may be accomplished in a high-throughput, large-scale automated manner, by using existing mass spectrometric profiling techniques and art well known in the fields of static proteomics and static organeomics, without the need for additional biochemical preparative steps or analytic/instrumental devices.

Technology

Technique for Measuring Dynamic Proteomics



SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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